

FIG. 1

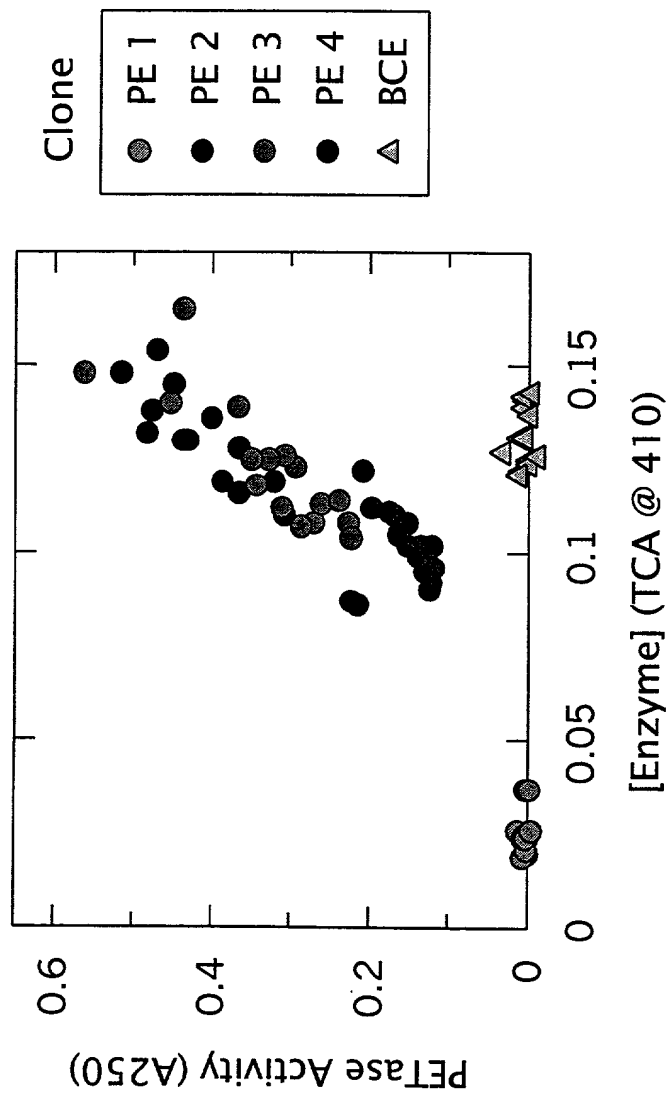


FIG. 2

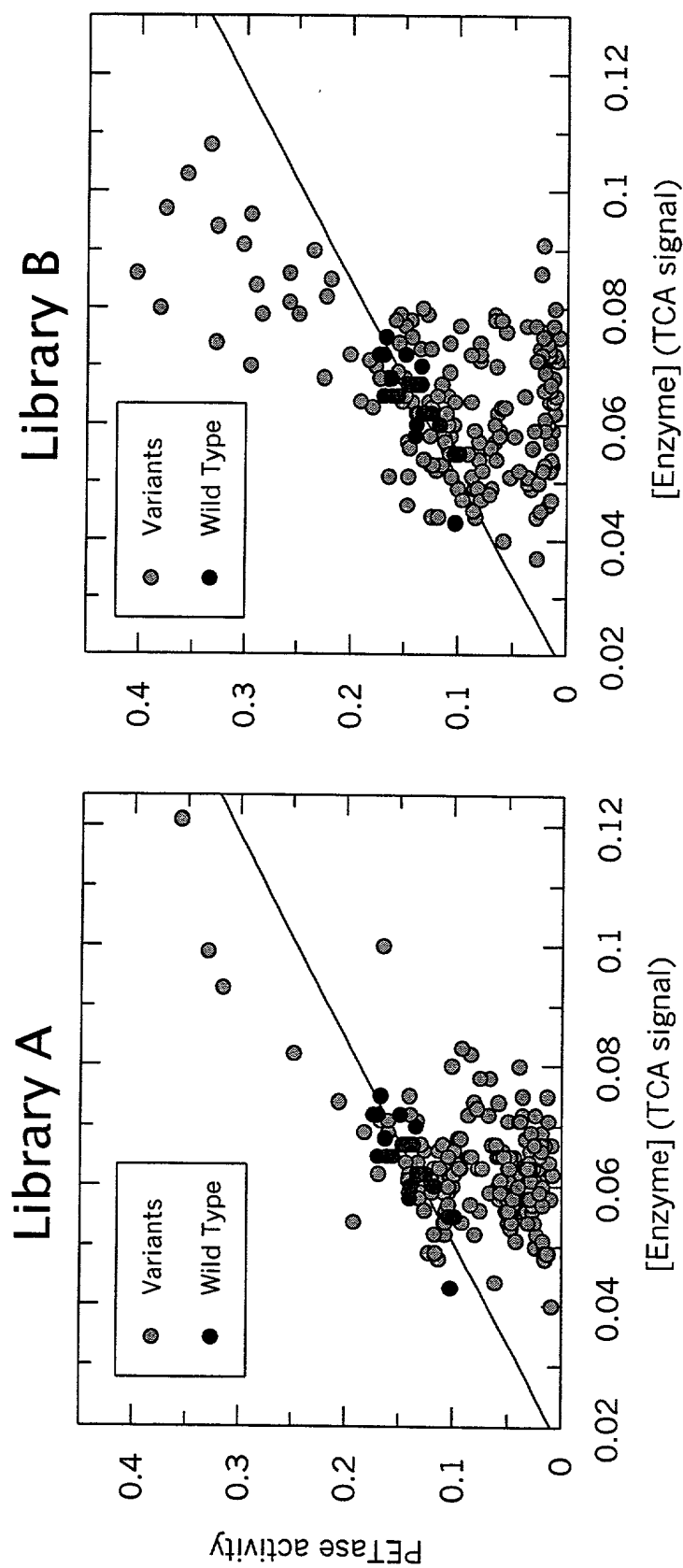


FIG. 3

FIG. 4

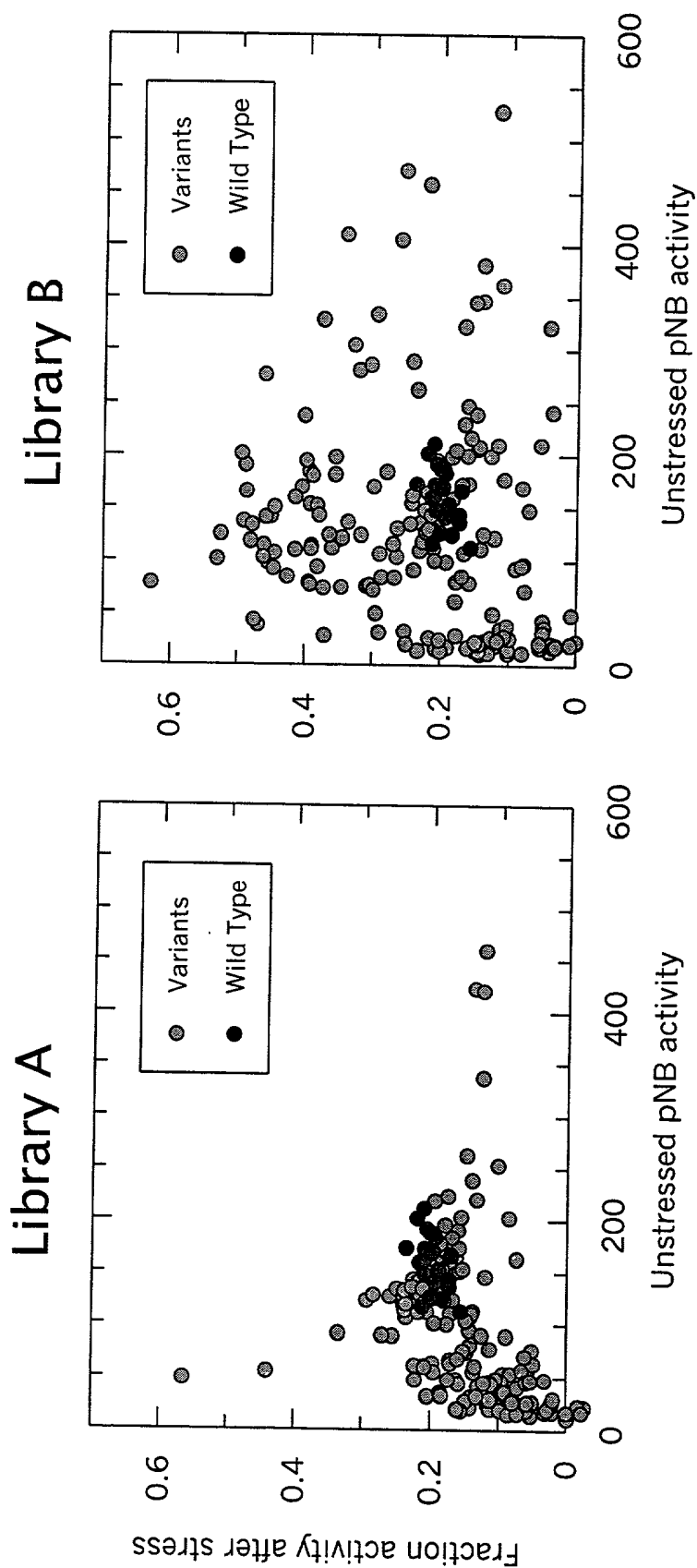


FIG. 5

FIG. 6

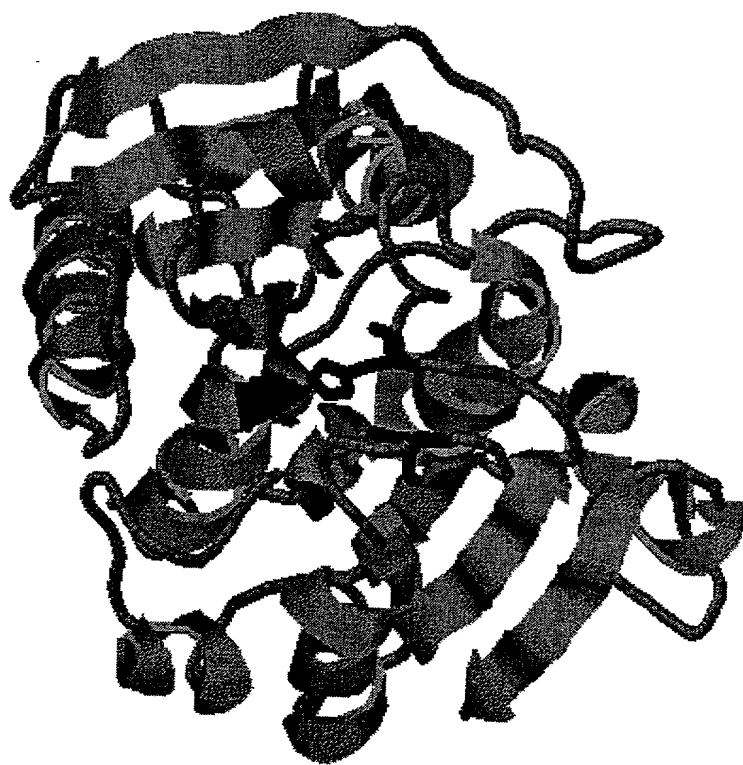


FIG. 7

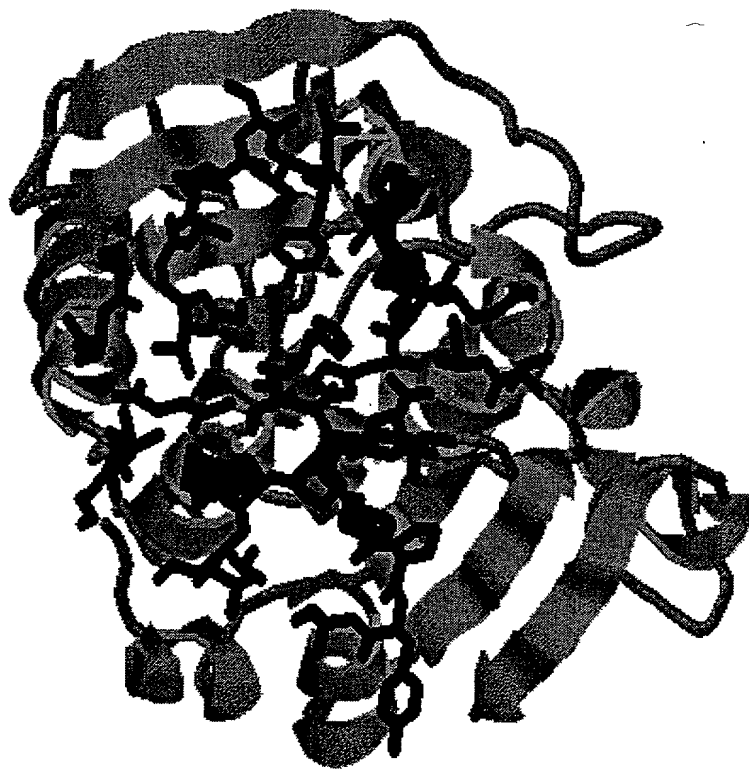


FIG. 8

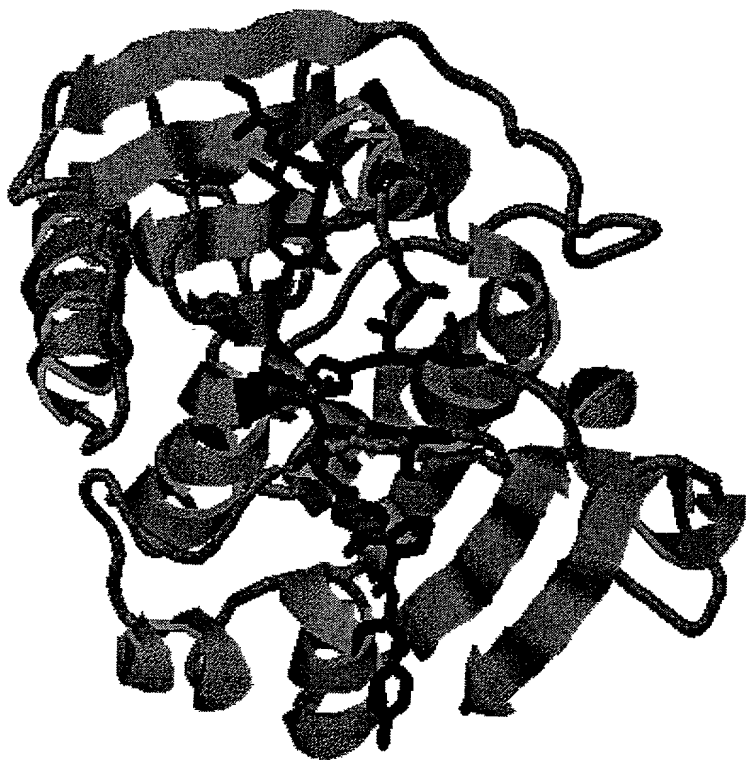


FIG. 9



FIG. 10

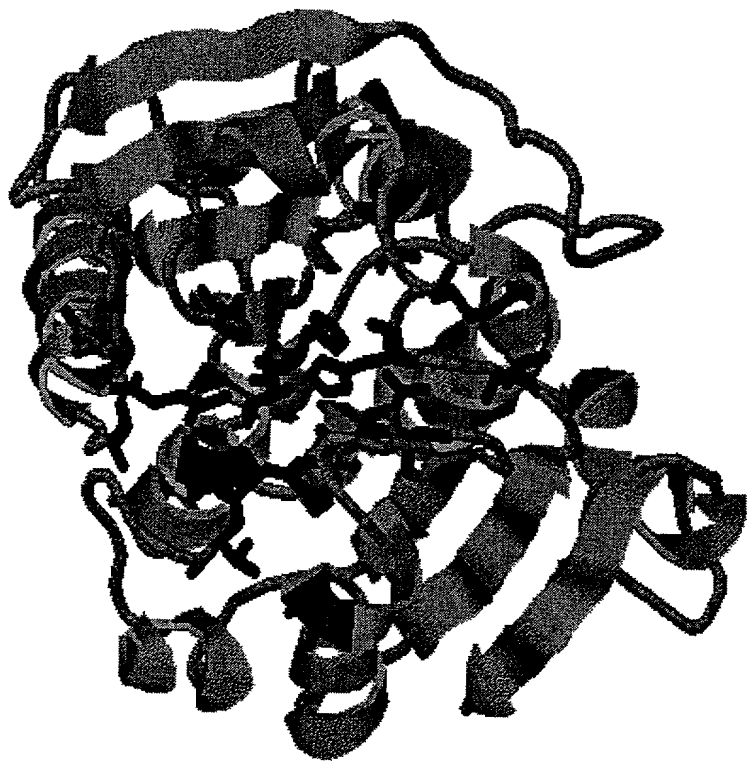


FIG. 11

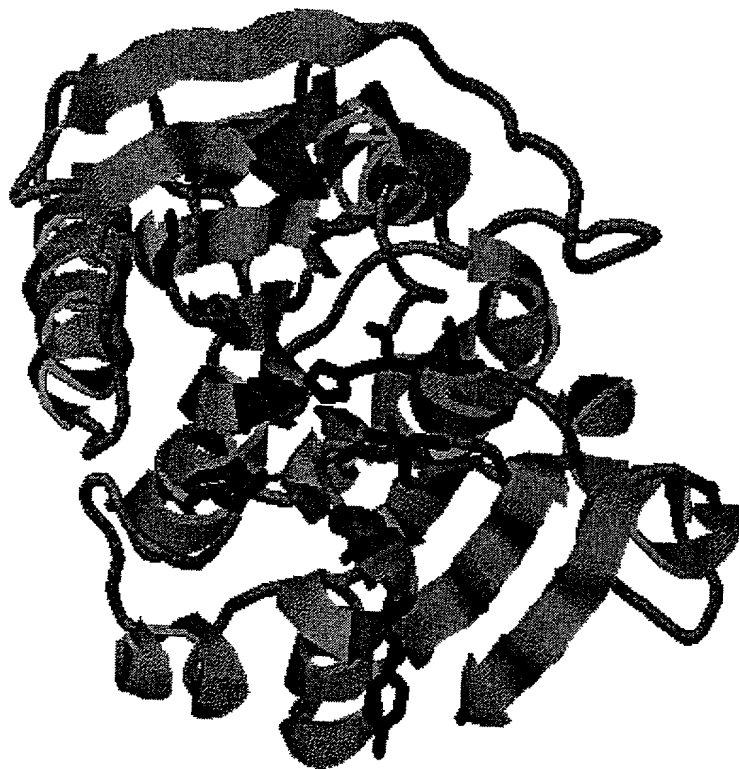


FIG. 12



FIG. 13

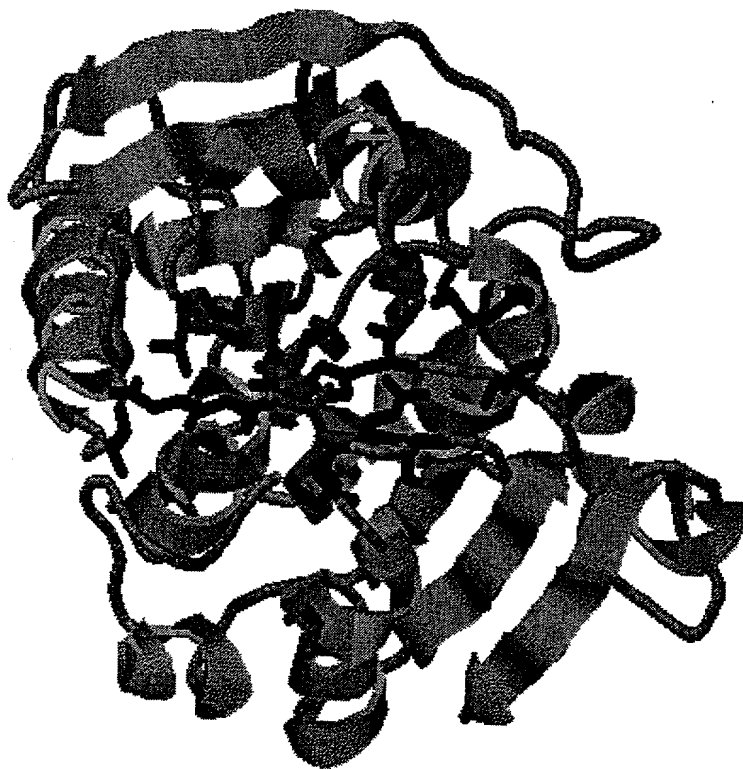


FIG. 14



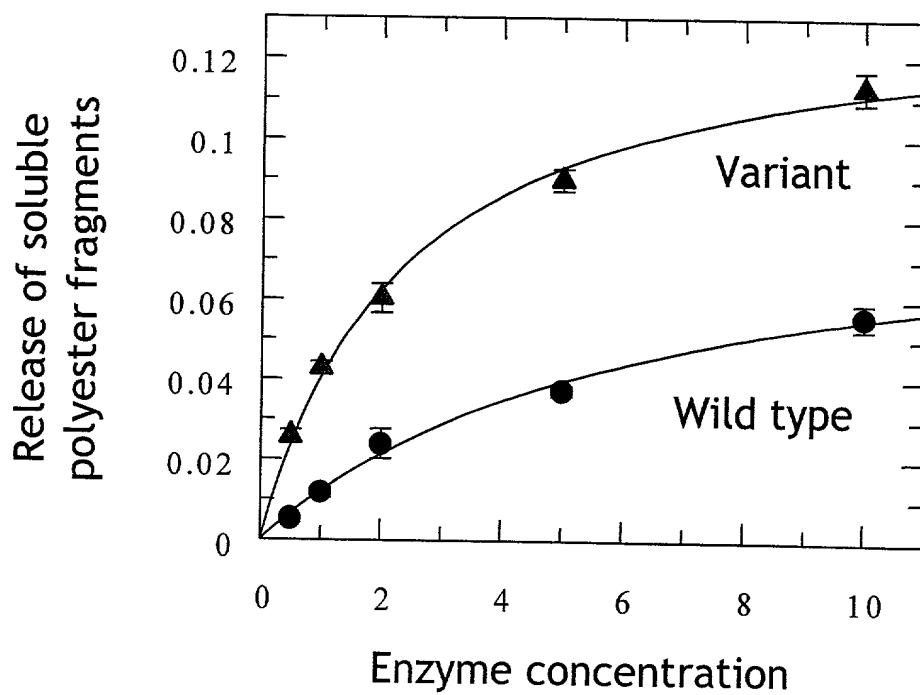


FIG. 15

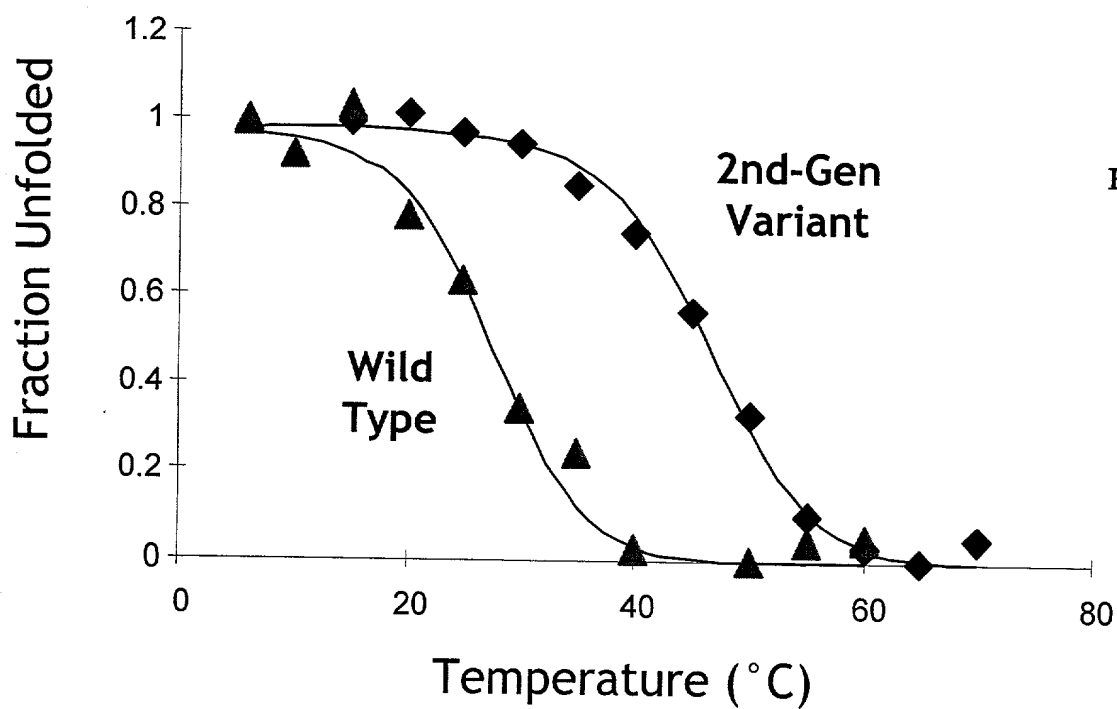


FIG. 16

lipasewtgene.seq

Created: Tuesday, February 01, 2000 2:19 PM

10 20 30 40

TGGCGGCCTCTTGCCTGTCCGTCTGTGCCACTGTCGCGGC 40  
GGCTCCCCTGCCGGATACACCGGGAGCGCCATTTCCGGCT 80  
GTCGCCAATTTTCGACCGCAGTGGCCCCTACACCACCAGCA 120  
GCCAGAGCGAGGGGGCCGAGCTGTGCGCATCTATCGGCCCCG 160  
CGACCTGGGTCAGGGGGGGCGTGCGTCATCCGGTGATTCTC 200

210 220 230 240

TGGGGCAATGGCACCGGTGCCGGGGCCGTCCACCTATGCCG 240  
GCTTGCTATCGCACTGGGCAAGCCACGGTTTCGTGGTGGC 280  
GGCGGCGGAAACCTCCAATGCCGGTACCGGGCGGGAAATG 320  
CTCGCCTGCCTGGACTATCTGGTACGTGAGAACGACACCC 360  
CGTACGGCACCTATTCCGGCAAGCTCAATACCGGGCGAGT 400

410 420 430 440

CGGCACTTCTGGGCATTCCCAGGGTGGTGGCGGCTCGATC 440  
ATGGCCGGGCAGGATACGAGGGTGCGTACCACGGCGCCGA 480  
TCCAGCCCTACACCCTCGGCCTGGGGCACGACAGCGCCTC 520  
GCAGCGGCGGCAGCAGGGGGCCGATGTTCCCTGATGTCCGGT 560  
GGCGGTGACACCATCGCCTTTCCCTACCTCAACGCTCAGC 600

610 620 630 640

CGGTCTACCGGCGTGCCAATGTGCCGGTGTTCTGGGGCGA 640  
ACGGCGTTACGTCAGCCACTTCGAGCCGGTCGGTAGCGGT 680  
GGGGCCTATCGCGGCCCCGAGCACGGCATGGTTCCGCTTCC 720  
AGCTGATGGATGACCAAGACGCCCGCGCTACCTTCTACGG 760  
CGCGCAGTGCAGTCTGTGCACCAGCCTGCTGTGGTCGGTC 800

810 820 830 840

GAGCGCCGCGGGCTTTAA 818

Fig. 17

lipasewtgene Map.MPD (1 &gt; 818) Site and Sequence

Enzymes : All 515 enzymes (No Filter)

Settings : Circular, Certain Sites Only, Standard Genetic Code

TGGCGGCCTCTTGCCTGTCCGTCTGTGCCACTGTGCGGGCGGCTCCCCTGCCGGATACACCGG 63  
Met Ala Ala Ser Cys Leu Ser Val Cys Ala Thr Val Ala Ala Ala Pro Leu Pro Asp Thr Pro

GAGCGCCATTTCCGGCTGTGCGCAATTTTCGACCGCAGTGGCCCCCTACACCACCAGCAGCCAGA 126  
Gly Ala Pro Phe Pro Ala Val Ala Asn Phe Asp Arg Ser Gly Pro Tyr Thr Thr Ser Ser Gln

GCGAGGGGGCCGAGCTGTGCGATCTATCGGCCCCGCGACCTGGGTCAGGGGGGGCGTGCGTCATC 189  
Ser Glu Gly Pro Ser Cys Arg Ile Tyr Arg Pro Arg Asp Leu Gly Gln Gly Gly Val Arg His

CGGTGATTCTCTGGGGCAATGGCACCGGTGCCGGGGCCGTCCACCTATGCCGGCTTGCTATCGC 252  
Pro Val Ile Leu Trp Gly Asn Gly Thr Gly Ala Gly Pro Ser Thr Tyr Ala Gly Leu Leu Ser

ACTGGGCAAGCCACGGTTTTCGTGGTGGCGGGCGGCGAAACCTCCAATGCCGGTACCGGGCGGG 315  
His Trp Ala Ser His Gly Phe Val Val Ala Ala Ala Glu Thr Ser Asn Ala Gly Thr Gly Arg

AAATGCTCGCCTGCCTGGACTATCTGGTACGTGAGAACGACACCCCCTACGGCACCTATTCCG 378  
Glu Met Leu Ala Cys Leu Asp Tyr Leu Val Arg Glu Asn Asp Thr Pro Tyr Gly Thr Tyr Ser

GCAAGCTCAATACCGGGCGAGTCGGCACTTCTGGGCATTCCCAGGGTGGTGGCGGCTCGATCA 441  
Gly Lys Leu Asn Thr Gly Arg Val Gly Thr Ser Gly His Ser Gln Gly Gly Gly Ser Ile

TGGCCGGGCAGGATACGAGGGTGC GTACCACGGCGCCGATCCAGCCCTACACCCTCGGCCTGG 504  
Met Ala Gly Gln Asp Thr Arg Val Arg Thr Thr Ala Pro Ile Gln Pro Tyr Thr Leu Gly Leu

GGCACGACAGCGCCTCGCAGCGGCGGCAGCAGGGGCCGATGTTCTGATGTCCGGTGGCGGTG 567  
Gly His Asp Ser Ala Ser Gln Arg Arg Gln Gln Gly Pro Met Phe Leu Met Ser Gly Gly Gly

ACACCATCGCCTTTCCCTACCTCAACGCTCAGCCGGTCTACCGGCGTGCCAATGTGCCGGTGT 630  
Asp Thr Ile Ala Phe Pro Tyr Leu Asn Ala Gln Pro Val Tyr Arg Arg Ala Asn Val Pro Val

TCTGGGGCGAACGGCGTTACGTCAGCCACTTCGAGCCGGTTCGGTAGCGGTGGGGCCTATCGCG 693  
Phe Trp Gly Glu Arg Arg Tyr Val Ser His Phe Glu Pro Val Gly Ser Gly Gly Ala Tyr Arg

GCCCGAGCACGGCATGGTTCCGCTTCCAGCTGATGGATGACCAAGACGCCCGCGCTACCTTCT 756  
Gly Pro Ser Thr Ala Trp Phe Arg Phe Gln Leu Met Asp Asp Gln Asp Ala Arg Ala Thr Phe

ACGGCGCGCAGTGCAGTCTGTGCACCAGCCTGCTGTGGTCGGTCGAGCGCCGCGGGCTTTAA 818  
Tyr Gly Ala Gln Cys Ser Leu Cys Thr Ser Leu Leu Trp Ser Val Glu Arg Arg Gly Leu •

Fig 18